

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ullrich, Axel  
Alves, Frauke
- (ii) TITLE OF INVENTION: MCK-10, A Novel Receptor Tyrosine Kinase
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pennie & Edmonds  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/153,397  
(B) FILING DATE: 16-NOV-1993  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Coruzzi, Laura A.  
(B) REGISTRATION NUMBER: 30,742  
(C) REFERENCE/DOCKET NUMBER: 7683-031
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (212) 790-9090  
(B) TELEFAX: (212) 869-9741/8864  
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3962 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 321..3077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGGCCTGAG ACTGGGGTGA CTGGGACCTA AGAGAATCCT GAGCTGGAGG CCCCCGACAG	60
CTGCTCTCGG GAGCCGCCTC CCGACACCCG AGCCCCGCCG GCGCCTCCCG CTCCCGGCTC	120
CCGGCTCCTG GCTCCCTCCG CCTCCCCCGC CCCTCGCCCC GCCGCCGAAG AGGCCCCGCT	180
CCCGGGTCGG ACGCCTGGGT CTGCCGGGAA GAGCGATGAG AGGTGTCTGA AGGTGGCTAT	240
TCACTGAGCG ATGGGGTTGG ACTTGAAGGA ATGCCAAGAG ATGCTGCCCC CACCCCCTTA	300
GGCCCGAGGG ATCAGGAGCT ATG GGA CCA GAG GCC CTG TCA TCT TTA CTG	350
Met Gly Pro Glu Ala Leu Ser Ser Leu Leu	
1 5 10	
CTG CTG CTC TTG GTG GCA AGT GGA GAT GCT GAC ATG AAG GGA CAT TTT	398
Leu Leu Leu Leu Val Ala Ser Gly Asp Ala Asp Met Lys Gly His Phe	
15 20 25	
GAT CCT GCC AAG TGC CGC TAT GCC CTG GGC ATG CAG GAC CGG ACC ATC	446
Asp Pro Ala Lys Cys Arg Tyr Ala Leu Gly Met Gln Asp Arg Thr Ile	
30 35 40	
CCA GAC AGT GAC ATC TCT GCT TCC AGC TCC TGG TCA GAT TCC ACT GCC	494
Pro Asp Ser Asp Ile Ser Ala Ser Ser Ser Trp Ser Asp Ser Thr Ala	
45 50 55	
GCC CGC CAC AGC AGG TTG GAG AGC AGT GAC GGG GAT GGG GCC TGG TGC	542
Ala Arg His Ser Arg Leu Glu Ser Ser Asp Gly Asp Gly Ala Trp Cys	
60 65 70	
CCC GCA GGG TCG GTG TTT CCC AAG GAG GAG GAG TAC TTG CAG GTG GAT	590
Pro Ala Gly Ser Val Phe Pro Lys Glu Glu Glu Tyr Leu Gln Val Asp	
75 80 85 90	
CTA CAA CGA CTC CAC CTG GTG GCT CTG GTG GGC ACC CAG GGA CGG CAT	638
Leu Gln Arg Leu His Leu Val Ala Leu Val Gly Thr Gln Gly Arg His	
95 100 105	
GCC GGG GGC CTG GGC AAG GAG TTC TCC CGG AGC TAC CGG CTG CGT TAC	686
Ala Gly Gly Leu Gly Lys Glu Phe Ser Arg Ser Tyr Arg Leu Arg Tyr	
110 115 120	
TCC CGG GAT GGT CGC CGC TGG ATG GGC TGG AAG GAC CGC TGG GGT CAG	734
Ser Arg Asp Gly Arg Arg Trp Met Gly Trp Lys Asp Arg Trp Gly Gln	
125 130 135	
GAG GTG ATC TCA GGC AAT GAG GAC CCT GAG GGA GTG GTG CTG AAG GAC	782
Glu Val Ile Ser Gly Asn Glu Asp Pro Glu Gly Val Val Leu Lys Asp	
140 145 150	



ACC TTC CCG CCA GCC CCC TGG TGG CCG CCT GGC CCA CCT CCC ACC AAC Thr Phe Pro Pro Ala Pro Trp Trp Pro Pro Gly Pro Pro Pro Thr Asn 380 385 390	1502
TTC AGC AGC TTG GAG CTG GAG CCC AGA GGC CAG CAG CCC GTG GCC AAG Phe Ser Ser Leu Glu Leu Glu Pro Arg Gly Gln Gln Pro Val Ala Lys 395 400 405 410	1550
GCC GAG GGG AGC CCG ACC GCC ATC CTC ATC GGC TGC CTG GTG GCC ATC Ala Glu Gly Ser Pro Thr Ala Ile Leu Ile Gly Cys Leu Val Ala Ile 415 420 425	1598
ATC CTG CTC CTG CTG CTC ATC ATT GCC CTC ATG CTC TGG CGG CTG CAC Ile Leu Leu Leu Leu Leu Ile Ile Ala Leu Met Leu Trp Arg Leu His 430 435 440	1646
TGG CGC AGG CTC CTC AGC AAG GCT GAA CGG AGG GTG TTG GAA GAG GAG Trp Arg Arg Leu Leu Ser Lys Ala Glu Arg Arg Val Leu Glu Glu Glu 445 450 455	1694
CTG ACG GTT CAC CTC TCT GTC CCT GGG GAC ACT ATC CTC ATC AAC AAC Leu Thr Val His Leu Ser Val Pro Gly Asp Thr Ile Leu Ile Asn Asn 460 465 470	1742
CGC CCA GGT CCT AGA GAG CCA CCC CCG TAC CAG GAG CCC CGG CCT CGT Arg Pro Gly Pro Arg Glu Pro Pro Pro Tyr Gln Glu Pro Arg Pro Arg 475 480 485 490	1790
GGG AAT CCG CCC CAC TCC GCT CCC TGT GTC CCC AAT GGC TCT GCG TTG Gly Asn Pro Pro His Ser Ala Pro Cys Val Pro Asn Gly Ser Ala Leu 495 500 505	1838
CTG CTC TCC AAT CCA GCC TAC CGC CTC CTT CTG GCC ACT TAC GCC CGT Leu Leu Ser Asn Pro Ala Tyr Arg Leu Leu Leu Ala Thr Tyr Ala Arg 510 515 520	1886
CCC CCT CGA GGC CCG GGC CCC CCC ACA CCC GCC TGG GCC AAA CCC ACC Pro Pro Arg Gly Pro Gly Pro Pro Thr Pro Ala Trp Ala Lys Pro Thr 525 530 535	1934
AAC ACC CAG GCC TAC AGT GGG GAC TAT ATG GAG CCT GAG AAG CCA GGC Asn Thr Gln Ala Tyr Ser Gly Asp Tyr Met Glu Pro Glu Lys Pro Gly 540 545 550	1982
GCC CCG CTT CTG CCC CCA CCT CCC CAG AAC AGC GTC CCC CAT TAT GCC Ala Pro Leu Leu Pro Pro Pro Pro Gln Asn Ser Val Pro His Tyr Ala 555 560 565 570	2030
GAG GCT GAC ATT GTT ACC CTG CAG GGC GTC ACC GGG GGC AAC ACC TAT Glu Ala Asp Ile Val Thr Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr 575 580 585	2078
GCT GTG CCT GCA CTG CCC CCA GGG GCA GTC GGG GAT GGG CCC CCC AGA Ala Val Pro Ala Leu Pro Pro Gly Ala Val Gly Asp Gly Pro Pro Arg 590 595 600	2126

GTG GAT TTC CCT CGA TCT CGA CTC CGC TTC AAG GAG AAG CTT GGC GAG Val Asp Phe Pro Arg Ser Arg Leu Arg Phe Lys Glu Lys Leu Gly Glu 605 610 615	2174
GGC CAG TTT GGG GAG GTG CAC CTG TGT GAG GTC GAC AGC CCT CAA GAT Gly Gln Phe Gly Glu Val His Leu Cys Glu Val Asp Ser Pro Gln Asp 620 625 630	2222
CTG GTC AGT CTT GAT TTC CCC CTT AAT GTG CGT AAG GGA CAC CCT TTG Leu Val Ser Leu Asp Phe Pro Leu Asn Val Arg Lys Gly His Pro Leu 635 640 645 650	2270
CTG GTA GCT GTC AAG ATC TTA CGG CCA GAT GCC ACC AAG AAT GCC AGC Leu Val Ala Val Lys Ile Leu Arg Pro Asp Ala Thr Lys Asn Ala Ser 655 660 665	2318
TTC TCC TTG TTC TCC AGG AAT GAT TTC CTG AAA GAG GTG AAG ATC ATG Phe Ser Leu Phe Ser Arg Asn Asp Phe Leu Lys Glu Val Lys Ile Met 670 675 680	2366
TCG AGG CTC AAG GAC CCC AAC ATC ATT CGG CTG CTG GGC GTG TGT GTG Ser Arg Leu Lys Asp Pro Asn Ile Ile Arg Leu Leu Gly Val Cys Val 685 690 695	2414
CAG GAC GAC CCC CTC TGC ATG ATT ACT GAC TAC ATG GAG AAC GGC GAC Gln Asp Asp Pro Leu Cys Met Ile Thr Asp Tyr Met Glu Asn Gly Asp 700 705 710	2462
CTC AAC CAG TTC CTC AGT GCC CAC CAG CTG GAG GAC AAG GCA GCC GAG Leu Asn Gln Phe Leu Ser Ala His Gln Leu Glu Asp Lys Ala Ala Glu 715 720 725 730	2510
GGG GCC CCT GGG GAC GGG CAG GCT GCG CAG GGG CCC ACC ATC AGC TAC Gly Ala Pro Gly Asp Gly Gln Ala Ala Gln Gly Pro Thr Ile Ser Tyr 735 740 745	2558
CCA ATG CTG CTG CAT GTG GCA GCC CAG ATC GCC TCC GGC ATG CGC TAT Pro Met Leu Leu His Val Ala Ala Gln Ile Ala Ser Gly Met Arg Tyr 750 755 760	2606
CTG GCC ACA CTC AAC TTT GTA CAT CGG GAC CTG GCC ACG CGG AAC TGC Leu Ala Thr Leu Asn Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys 765 770 775	2654
CTA GTT GGG GAA AAT TTC ACC ATC AAA ATC GCA GAC TTT GGC ATG AGC Leu Val Gly Glu Asn Phe Thr Ile Lys Ile Ala Asp Phe Gly Met Ser 780 785 790	2702
CGG AAC CTC TAT GCT GGG GAC TAT TAC CGT GTG CAG GGC CGG GCA GTG Arg Asn Leu Tyr Ala Gly Asp Tyr Tyr Arg Val Gln Gly Arg Ala Val 795 800 805 810	2750
CTG CCC ATC CGC TGG ATG GCC TGG GAG TGC ATC CTC ATG GGG AAG TTC Leu Pro Ile Arg Trp Met Ala Trp Glu Cys Ile Leu Met Gly Lys Phe 815 820 825	2798

ACG ACT GCG AGT GAC GTG TGG GCC TTT GGT GTG ACC CTG TGG GAG GTG Thr Thr Ala Ser Asp Val Trp Ala Phe Gly Val Thr Leu Trp Glu Val 830 835 840	2846
CTG ATG CTC TGT AGG GCC CAG CCC TTT GGG CAG CTC ACC GAC GAG CAG Leu Met Leu Cys Arg Ala Gln Pro Phe Gly Gln Leu Thr Asp Glu Gln 845 850 855	2894
GTC ATC GAG AAC GCG GGG GAG TTC TTC CGG GAC CAG GGC CGG CAG GTG Val Ile Glu Asn Ala Gly Glu Phe Phe Arg Asp Gln Gly Arg Gln Val 860 865 870	2942
TAC CTG TCC CGG CCG CCT GCC TGC CCG CAG GGC CTA TAT GAG CTG ATG Tyr Leu Ser Arg Pro Pro Ala Cys Pro Gln Gly Leu Tyr Glu Leu Met 875 880 885 890	2990
CTT CGG TGC TGG AGC CGG GAG TCT GAG CAG CGA CCA CCC TTT TCC CAG Leu Arg Cys Trp Ser Arg Glu Ser Glu Gln Arg Pro Pro Phe Ser Gln 895 900 905	3038
CTG CAT CGG TTC CTG GCA GAG GAT GCA CTC AAC ACG GTG TGAATCACAC Leu His Arg Phe Leu Ala Glu Asp Ala Leu Asn Thr Val 910 915	3087
ATCCAGCTGC CCCTCCCTCA GGGAGTGATC CAGGGGAAGC CAGTGACACT AAAACAAGAG	3147
GACACAATGG CACCTCTGCC CTTCCCCTCC CGACAGCCCA TCACCTCTAA TAGAGGCAGT	3207
GAGACTGCAG GTGGGCTGGG CCCACCCAGG GAGCTGATGC CCCTTCTCCC CTTCTTGGAC	3267
ACACTCTCAT GTCCCCTTCC TGTTCTTCTT TCCTAGAAGC CCCTGTCGCC CACCCAGCTG	3327
GTCCTGTGGA TGGGATCCTC TCCACCCTCC TCTAGCCATC CCTTGGGGAA GGGTGGGGAG	3387
AAATATAGGA TAGACACTGG ACATGGCCCA TTGGAGCACC TGGGCCCCAC TGGACAACAC	3447
TGATTCTTGG AGAGGTGGCT GCGCCCCAGC TTCTCTCTCC CTGTCACACA CTGGACCCCA	3507
CTGGCTGAGA ATCTGGGGGT GAGGAGGACA AGAAGGAGAG GAAAATGTTT CTTGTGCCT	3567
GCTCCTGTAC TTGTCCTCAG CTTGGGCTTC TTCCTCCTCC ATCACCTGAA AACTGGACC	3627
TGGGGGTAGC CCCGCCCCAG CCCTCAGTCA CCCCCACTTC CCACTTGCAG TCTTGTAGCT	3687
AGAACTTCTC TAAGCCTATA CGTTTCTGTG GAGTAAATAT TGGGATTGGG GGGAAAGAGG	3747
GAGCAACGGC CCATAGCCTT GGGGTTGGAC ATCTCTAGTG TAGCTGCCAC ATTGATTTTT	3807
CTATAATCAC TTGGGGTTTG TACATTTTTG GGGGGAGAGA CACAGATTTT TACACTAATA	3867
TATGGACCTA GCTTGAGGCA ATTTTAATCC CCTGCACTAG GCAGGTAATA ATAAAGGTTG	3927
AGTTTTCCAC AAAAAAAAAA AAAAAACCGG AATTC	3962

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 919 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Pro Glu Ala Leu Ser Ser Leu Leu Leu Leu Leu Val Ala  
 1 5 10 15  
 Ser Gly Asp Ala Asp Met Lys Gly His Phe Asp Pro Ala Lys Cys Arg  
 20 25 30  
 Tyr Ala Leu Gly Met Gln Asp Arg Thr Ile Pro Asp Ser Asp Ile Ser  
 35 40 45  
 Ala Ser Ser Ser Trp Ser Asp Ser Thr Ala Ala Arg His Ser Arg Leu  
 50 55 60  
 Glu Ser Ser Asp Gly Asp Gly Ala Trp Cys Pro Ala Gly Ser Val Phe  
 65 70 75 80  
 Pro Lys Glu Glu Glu Tyr Leu Gln Val Asp Leu Gln Arg Leu His Leu  
 85 90 95  
 Val Ala Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly Leu Gly Lys  
 100 105 110  
 Glu Phe Ser Arg Ser Tyr Arg Leu Arg Tyr Ser Arg Asp Gly Arg Arg  
 115 120 125  
 Trp Met Gly Trp Lys Asp Arg Trp Gly Gln Glu Val Ile Ser Gly Asn  
 130 135 140  
 Glu Asp Pro Glu Gly Val Val Leu Lys Asp Leu Gly Pro Pro Met Val  
 145 150 155 160  
 Ala Arg Leu Val Arg Phe Tyr Pro Arg Ala Asp Arg Val Met Ser Val  
 165 170 175  
 Cys Leu Arg Val Glu Leu Tyr Gly Cys Leu Trp Arg Asp Gly Leu Leu  
 180 185 190  
 Ser Tyr Thr Ala Pro Val Gly Gln Thr Met Tyr Leu Ser Glu Ala Val  
 195 200 205  
 Tyr Leu Asn Asp Ser Thr Tyr Asp Gly His Thr Val Gly Gly Leu Gln  
 210 215 220  
 Tyr Gly Gly Leu Gly Gln Leu Ala Asp Gly Val Val Gly Leu Asp Asp  
 225 230 235 240  
 Phe Arg Lys Ser Gln Glu Leu Arg Val Trp Pro Gly Tyr Asp Tyr Val  
 245 250 255  
 Gly Trp Ser Asn His Ser Phe Ser Ser Gly Tyr Val Glu Met Glu Phe  
 260 265 270

Glu Phe Asp Arg Leu Arg Ala Phe Gln Ala Met Gln Val His Cys Asn  
275 280 285

Asn Met His Thr Leu Gly Ala Arg Leu Pro Gly Gly Val Glu Cys Arg  
290 295 300

Phe Arg Arg Gly Pro Ala Met Ala Trp Glu Gly Glu Pro Met Arg His  
305 310 315 320

Asn Leu Gly Gly Asn Leu Gly Asp Pro Arg Ala Arg Ala Val Ser Val  
325 330 335

Pro Leu Gly Gly Arg Val Ala Arg Phe Leu Gln Cys Arg Phe Leu Phe  
340 345 350

Ala Gly Pro Trp Leu Leu Phe Ser Glu Ile Ser Phe Ile Ser Asp Val  
355 360 365

Val Asn Asn Ser Ser Pro Ala Leu Gly Gly Thr Phe Pro Pro Ala Pro  
370 375 380

Trp Trp Pro Pro Gly Pro Pro Pro Thr Asn Phe Ser Ser Leu Glu Leu  
385 390 395 400

Glu Pro Arg Gly Gln Gln Pro Val Ala Lys Ala Glu Gly Ser Pro Thr  
405 410 415

Ala Ile Leu Ile Gly Cys Leu Val Ala Ile Ile Leu Leu Leu Leu Leu  
420 425 430

Ile Ile Ala Leu Met Leu Trp Arg Leu His Trp Arg Arg Leu Leu Ser  
435 440 445

Lys Ala Glu Arg Arg Val Leu Glu Glu Glu Leu Thr Val His Leu Ser  
450 455 460

Val Pro Gly Asp Thr Ile Leu Ile Asn Asn Arg Pro Gly Pro Arg Glu  
465 470 475 480

Pro Pro Pro Tyr Gln Glu Pro Arg Pro Arg Gly Asn Pro Pro His Ser  
485 490 495

Ala Pro Cys Val Pro Asn Gly Ser Ala Leu Leu Leu Ser Asn Pro Ala  
500 505 510

Tyr Arg Leu Leu Leu Ala Thr Tyr Ala Arg Pro Pro Arg Gly Pro Gly  
515 520 525

Pro Pro Thr Pro Ala Trp Ala Lys Pro Thr Asn Thr Gln Ala Tyr Ser  
530 535 540

Gly Asp Tyr Met Glu Pro Glu Lys Pro Gly Ala Pro Leu Leu Pro Pro  
545 550 555 560

Pro Pro Gln Asn Ser Val Pro His Tyr Ala Glu Ala Asp Ile Val Thr  
565 570 575



Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ala Val Pro Ala Leu Pro  
 580 585 590  
 Pro Gly Ala Val Gly Asp Gly Pro Pro Arg Val Asp Phe Pro Arg Ser  
 595 600 605  
 Arg Leu Arg Phe Lys Glu Lys Leu Gly Glu Gly Gln Phe Gly Glu Val  
 610 615 620  
 His Leu Cys Glu Val Asp Ser Pro Gln Asp Leu Val Ser Leu Asp Phe  
 625 630 635 640  
 Pro Leu Asn Val Arg Lys Gly His Pro Leu Leu Val Ala Val Lys Ile  
 645 650 655  
 Leu Arg Pro Asp Ala Thr Lys Asn Ala Ser Phe Ser Leu Phe Ser Arg  
 660 665 670  
 Asn Asp Phe Leu Lys Glu Val Lys Ile Met Ser Arg Leu Lys Asp Pro  
 675 680 685  
 Asn Ile Ile Arg Leu Leu Gly Val Cys Val Gln Asp Asp Pro Leu Cys  
 690 695 700  
 Met Ile Thr Asp Tyr Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser  
 705 710 715 720  
 Ala His Gln Leu Glu Asp Lys Ala Ala Glu Gly Ala Pro Gly Asp Gly  
 725 730 735  
 Gln Ala Ala Gln Gly Pro Thr Ile Ser Tyr Pro Met Leu Leu His Val  
 740 745 750  
 Ala Ala Gln Ile Ala Ser Gly Met Arg Tyr Leu Ala Thr Leu Asn Phe  
 755 760 765  
 Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Phe  
 770 775 780  
 Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg Asn Leu Tyr Ala Gly  
 785 790 795 800  
 Asp Tyr Tyr Arg Val Gln Gly Arg Ala Val Leu Pro Ile Arg Trp Met  
 805 810 815  
 Ala Trp Glu Cys Ile Leu Met Gly Lys Phe Thr Thr Ala Ser Asp Val  
 820 825 830  
 Trp Ala Phe Gly Val Thr Leu Trp Glu Val Leu Met Leu Cys Arg Ala  
 835 840 845  
 Gln Pro Phe Gly Gln Leu Thr Asp Glu Gln Val Ile Glu Asn Ala Gly  
 850 855 860  
 Glu Phe Phe Arg Asp Gln Gly Arg Gln Val Tyr Leu Ser Arg Pro Pro  
 865 870 875 880

Ala Cys Pro Gln Gly Leu Tyr Glu Leu Met Leu Arg Cys Trp Ser Arg  
885 890 895

Glu Ser Glu Gln Arg Pro Pro Phe Ser Gln Leu His Arg Phe Leu Ala  
900 905 910

Glu Asp Ala Leu Asn Thr Val  
915

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 370..2934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCACGAGCGG CACGAGTCCA TGATCTCTTT CCATCCTCCC TTTCCTGTTT GCTCACTTCT	60
TTTCTTGCTC ATCTTGGAGA CTGTGCAATC CCAGATTAAC TACAAACAGA GAAGAGCTGG	120
TGATAGCTCC AGAGCTCAGA GAAAGGAGGT CTCTTTACAA GAAGTCTGGC TCTCAAAGCC	180
TCCATCAAGG GAGACCTACA AGTTGCCTGG GGTTCAGTGC TCTAGAAAGT TCCAAGGTTT	240
GTGGCTTGAA TTATTCTAAA GAAGCTGAAA TAATTGAAGA GAAGCAGAGG CCAGCTGTTT	300
TTGAGGATCC TGCTCCACAG AGAATGCTCT GCACCCGTTG ATACTCCAGT TCCAACACCA	360
TCTTCTGAG ATG ATC CTG ATT CCC AGA ATG CTC TTG GTG CTG TTC CTG	408
Met Ile Leu Ile Pro Arg Met Leu Leu Val Leu Phe Leu	
1 5 10	
CTG CTG CCT ATC TTG AGT TCT GCA AAA GCT CAG GTT AAT CCA GCT ATA	456
Leu Leu Pro Ile Leu Ser Ser Ala Lys Ala Gln Val Asn Pro Ala Ile	
15 20 25	
TGC CGC TAT CCT CTG GGC ATG TCA GGA GGC CAG ATT CCA GAT GAG GAC	504
Cys Arg Tyr Pro Leu Gly Met Ser Gly Gly Gln Ile Pro Asp Glu Asp	
30 35 40 45	
ATC ACA GCT TCC AGT CAG TGG TCA GAG TCC ACA GCT GCC AAA TAT GGA	552
Ile Thr Ala Ser Ser Gln Trp Ser Glu Ser Thr Ala Ala Lys Tyr Gly	
50 55 60	

AGG CTG GAC TCA GAA GAA GGG GAT GGA GCC TGG TGC CCT GAG ATT CCA	600
Arg Leu Asp Ser Glu Glu Gly Asp Gly Ala Trp Cys Pro Glu Ile Pro	
65 70 75	
GTG GAA CCT GAT GAC CTG AAG GAG TTT CTG CAG ATT GAC TTG CAC ACC	648
Val Glu Pro Asp Asp Leu Lys Glu Phe Leu Gln Ile Asp Leu His Thr	
80 85 90	
CTC CAT TTT ATC ACT CTG GTG GGG ACC CAG GGG CGC CAT GCA GGA GGT	696
Leu His Phe Ile Thr Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly	
95 100 105	
CAT GGC ATC GAG TTT GCC CCC ATG TAC AAG ATC AAT TAC AGT CGG GAT	744
His Gly Ile Glu Phe Ala Pro Met Tyr Lys Ile Asn Tyr Ser Arg Asp	
110 115 120 125	
GGC ACT CGC TGG ATC TCT TGG CGG AAC CGT CAT GGG AAA CAG GTG CTG	792
Gly Thr Arg Trp Ile Ser Trp Arg Asn Arg His Gly Lys Gln Val Leu	
130 135 140	
GAT GGA AAT AGT AAC CCC TAT GAC ATT TTC CTA AAG GAC TTG GAG CCG	840
Asp Gly Asn Ser Asn Pro Tyr Asp Ile Phe Leu Lys Asp Leu Glu Pro	
145 150 155	
CCC ATT GTA GCC AGA TTT GTC CGG TTC ATT CCA GTC ACC GAC CAC TCC	888
Pro Ile Val Ala Arg Phe Val Arg Phe Ile Pro Val Thr Asp His Ser	
160 165 170	
ATG AAT GTG TGT ATG AGA GTG GAG CTT TAC GGC TGT GTC TGG CTA GAT	936
Met Asn Val Cys Met Arg Val Glu Leu Tyr Gly Cys Val Trp Leu Asp	
175 180 185	
GGC TTG GTG TCT TAC AAT GCT CCA GCT GGG CAG CAG TTT GTA CTC CCT	984
Gly Leu Val Ser Tyr Asn Ala Pro Ala Gly Gln Gln Phe Val Leu Pro	
190 195 200 205	
GGA GGT TCC ATC ATT TAT CTG AAT GAT TCT GTC TAT GAT GGA GCT GTT	1032
Gly Gly Ser Ile Ile Tyr Leu Asn Asp Ser Val Tyr Asp Gly Ala Val	
210 215 220	
GGA TAC AGC ATG ACA GAA GGG CTA GGC CAA TTG ACC GAT GGT GTG TCT	1080
Gly Tyr Ser Met Thr Glu Gly Leu Gly Gln Leu Thr Asp Gly Val Ser	
225 230 235	
GGC CTG GAC GAT TTC ACC CAG ACC CAT GAA TAC CAC GTG TGG CCC GGC	1128
Gly Leu Asp Asp Phe Thr Gln Thr His Glu Tyr His Val Trp Pro Gly	
240 245 250	
TAT GAC TAT GTG GGC TGG CGG AAC GAG AGT GCC ACC AAT GGC TAC ATT	1176
Tyr Asp Tyr Val Gly Trp Arg Asn Glu Ser Ala Thr Asn Gly Tyr Ile	
255 260 265	
GAG ATC ATG TTT GAA TTT GAC CGC ATC AGG AAT TTC ACT ACC ATG AAG	1224
Glu Ile Met Phe Glu Phe Asp Arg Ile Arg Asn Phe Thr Thr Met Lys	
270 275 280 285	

GTC CAC TGC AAC AAC ATG TTT GCT AAA GGT GTG AAG ATC TTT AAG GAG Val His Cys Asn Asn Met Phe Ala Lys Gly Val Lys Ile Phe Lys Glu 290 295 300	1272
GTA CAG TGC TAC TTC CGC TCT GAA GCC AGT GAG TGG GAA CCT AAT GCC Val Gln Cys Tyr Phe Arg Ser Glu Ala Ser Glu Trp Glu Pro Asn Ala 305 310 315	1320
ATT TCC TTC CCC CTT GTC CTG GAT GAC GTC AAC CCC AGT GCT CGG TTT Ile Ser Phe Pro Leu Val Leu Asp Asp Val Asn Pro Ser Ala Arg Phe 320 325 330	1368
GTC ACG GTG CCT CTC CAC CAC CGA ATG GCC AGT GCC ATC AAG TGT CAA Val Thr Val Pro Leu His His Arg Met Ala Ser Ala Ile Lys Cys Gln 335 340 345	1416
TAC CAT TTT GCA GAT ACC TGG ATG ATG TTC AGT GAG ATC ACC TTC CAA Tyr His Phe Ala Asp Thr Trp Met Met Phe Ser Glu Ile Thr Phe Gln 350 355 360 365	1464
TCA GAT GCT GCA ATG TAC AAC AAC TCT GAA GCC CTG CCC ACC TCT CCT Ser Asp Ala Ala Met Tyr Asn Asn Ser Glu Ala Leu Pro Thr Ser Pro 370 375 380	1512
ATG GCA CCC ACA ACC TAT GAT CCA ATG CTT AAA GTT GAT GAC AGC AAC Met Ala Pro Thr Thr Tyr Asp Pro Met Leu Lys Val Asp Asp Ser Asn 385 390 395	1560
ACT CGG ATC CTG ATT GGC TGC TTG GTG GCC ATC ATC TTT ATC CTC CTG Thr Arg Ile Leu Ile Gly Cys Leu Val Ala Ile Ile Phe Ile Leu Leu 400 405 410	1608
GCC ATC ATT GTC ATC ATC CTC TGG AGG CAG TTC TGG CAG AAA ATG CTG Ala Ile Ile Val Ile Ile Leu Trp Arg Gln Phe Trp Gln Lys Met Leu 415 420 425	1656
GAG AAG GCT TCT CGG AGG ATG CTG GAT GAT GAA ATG ACA GTC AGC CTT Glu Lys Ala Ser Arg Arg Met Leu Asp Asp Glu Met Thr Val Ser Leu 430 435 440 445	1704
TCC CTG CCA AGT GAT TCT AGC ATG TTC AAC AAT AAC CGC TCC TCA TCA Ser Leu Pro Ser Asp Ser Ser Met Phe Asn Asn Asn Arg Ser Ser Ser 450 455 460	1752
CCT AGT GAA CAA GGG TCC AAC TCG ACT TAC GAT CGC ATC TTT CCC CTT Pro Ser Glu Gln Gly Ser Asn Ser Thr Tyr Asp Arg Ile Phe Pro Leu 465 470 475	1800
CGC CCT GAC TAC CAG GAG CCA TCC AGG CTG ATA CGA AAA CTC CCA GAA Arg Pro Asp Tyr Gln Glu Pro Ser Arg Leu Ile Arg Lys Leu Pro Glu 480 485 490	1848
TTT GCT CCA GGG GAG GAG GAG TCA GGC TGC AGC GGT GTT GTG AAG CCA Phe Ala Pro Gly Glu Glu Glu Ser Gly Cys Ser Gly Val Val Lys Pro 495 500 505	1896

GTC CAG CCC AGT GGC CCT GAG GGG GTG CCC CAC TAT GCA GAG GCT GAC Val Gln Pro Ser Gly Pro Glu Gly Val Pro His Tyr Ala Glu Ala Asp 510 515 520 525	1944
ATA GTG AAC CTC CAA GGA GTG ACA GGA GGC AAC ACA TAC TCA GTG CCT Ile Val Asn Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ser Val Pro 530 535 540	1992
GCC GTC ACC ATG GAC CTG CTC TCA GGA AAA GAT GTG GCT GTG GAG GAG Ala Val Thr Met Asp Leu Leu Ser Gly Lys Asp Val Ala Val Glu Glu 545 550 555	2040
TTC CCC AGG AAA CTC CTA ACT TTC AAA GAG AAG CTG GGA GAA GGA CAG Phe Pro Arg Lys Leu Leu Thr Phe Lys Glu Lys Leu Gly Glu Gly Gln 560 565 570	2088
TTT GGG GAG GTT CAT CTC TGT GAA GTG GAG GGA ATG GAA AAA TTC AAA Phe Gly Glu Val His Leu Cys Glu Val Glu Gly Met Glu Lys Phe Lys 575 580 585	2136
GAC AAA GAT TTT GCC CTA GAT GTC AGT GCC AAC CAG CCT GTC CTG GTG Asp Lys Asp Phe Ala Leu Asp Val Ser Ala Asn Gln Pro Val Leu Val 590 595 600 605	2184
GCT GTG AAA ATG CTC CGA GCA GAT GCC AAC AAG AAT GCC AGG AAT GAT Ala Val Lys Met Leu Arg Ala Asp Ala Asn Lys Asn Ala Arg Asn Asp 610 615 620	2232
TTT CTT AAG GAG ATA AAG ATC ATG TCT CGG CTC AAG GAC CCA AAC ATC Phe Leu Lys Glu Ile Lys Ile Met Ser Arg Leu Lys Asp Pro Asn Ile 625 630 635	2280
ATC CAT CTA TTA TCT GTG TGT ATC ACT GAT GAC CCT CTC TGT ATG ATC Ile His Leu Leu Ser Val Cys Ile Thr Asp Asp Pro Leu Cys Met Ile 640 645 650	2328
ACT GAA TAC ATG GAG AAT GGA GAT CTC AAT CAG TTT CTT TCC CGC CAC Thr Glu Tyr Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser Arg His 655 660 665	2376
GAG CCC CCT AAT TCT TCC TCC AGC GAT GTA CGC ACT GTC AGT TAC ACC Glu Pro Pro Asn Ser Ser Ser Ser Asp Val Arg Thr Val Ser Tyr Thr 670 675 680 685	2424
AAT CTG AAG TTT ATG GCT ACC CAA ATT GCC TCT GGC ATG AAG TAC CTT Asn Leu Lys Phe Met Ala Thr Gln Ile Ala Ser Gly Met Lys Tyr Leu 690 695 700	2472
TCC TCT CTT AAT TTT GTT CAC CGA GAT CTG GCC ACA CGA AAC TGT TTA Ser Ser Leu Asn Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu 705 710 715	2520
GTG GGT AAG AAC TAC ACA ATC AAG ATA GCT GAC TTT GGA ATG AGC AGG Val Gly Lys Asn Tyr Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg 720 725 730	2568

AAC CTG TAC AGT GGT GAC TAT TAC CGG ATC CAG GGC CGG GCA GTG CTC Asn Leu Tyr Ser Gly Asp Tyr Tyr Arg Ile Gln Gly Arg Ala Val Leu 735 740 745	2616
CCT ATC CGC TGG ATG TCT TGG GAG AGT ATC TTG CTG GGC AAG TTC ACT Pro Ile Arg Trp Met Ser Trp Glu Ser Ile Leu Leu Gly Lys Phe Thr 750 755 760 765	2664
ACA GCA AGT GAT GTG TGG GCC TTT GGG GTT ACT TTG TGG GAG ACT TTC Thr Ala Ser Asp Val Trp Ala Phe Gly Val Thr Leu Trp Glu Thr Phe 770 775 780	2712
ACC TTT TGT CAA GAA CAG CCC TAT TCC CAG CTG TCA GAT GAA CAG GTT Thr Phe Cys Gln Glu Gln Pro Tyr Ser Gln Leu Ser Asp Glu Gln Val 785 790 795	2760
ATT GAG AAT ACT GGA GAG TTC TTC CGA GAC CAA GGG AGG CAG ACT TAC Ile Glu Asn Thr Gly Glu Phe Phe Arg Asp Gln Gly Arg Gln Thr Tyr 800 805 810	2808
CTC CCT CAA CCA GCC ATT TGT CCT GAC TCT GTG TAT AAG CTG ATG CTC Leu Pro Gln Pro Ala Ile Cys Pro Asp Ser Val Tyr Lys Leu Met Leu 815 820 825	2856
AGC TGC TGG AGA AGA GAT ACG AAG AAC CGT CCC TCA TTC CAA GAA ATC Ser Cys Trp Arg Arg Asp Thr Lys Asn Arg Pro Ser Phe Gln Glu Ile 830 835 840 845	2904
CAC CTT CTG CTC CTT CAA CAA GGC GAC GAG TGATGCTGTC AGTGCCTGGC His Leu Leu Leu Leu Gln Gln Gly Asp Glu 850 855	2954
CATGTTCTTA CGGCTCAGGT CCTCCCTACA AGACCTACCA CTCACCCATG CCTATGCCAC	3014
TCCATCTGGA CATTTAATGA AACTGAGAGA CAGAGGCTTG TTTGCTTTGC CCTCTTTTCC	3074
TGGTCACCCC CACTCCCTAC CCCTGACTCA TATATACTTT TTTTTTTTAC ATTAAAGAAC	3134
TAAAAAAAAA AAAAAAAAAAG GCG	3157

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ile	Leu	Ile	Pro	Arg	Met	Leu	Leu	Val	Leu	Phe	Leu	Leu	Leu	Pro
1				5					10					15	
Ile	Leu	Ser	Ser	Ala	Lys	Ala	Gln	Val	Asn	Pro	Ala	Ile	Cys	Arg	Tyr
		20					25						30		

Pro Leu Gly Met Ser Gly Gly Gln Ile Pro Asp Glu Asp Ile Thr Ala  
 35 40 45  
 Ser Ser Gln Trp Ser Glu Ser Thr Ala Ala Lys Tyr Gly Arg Leu Asp  
 50 55 60  
 Ser Glu Glu Gly Asp Gly Ala Trp Cys Pro Glu Ile Pro Val Glu Pro  
 65 70 75 80  
 Asp Asp Leu Lys Glu Phe Leu Gln Ile Asp Leu His Thr Leu His Phe  
 85 90 95  
 Ile Thr Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly His Gly Ile  
 100 105 110  
 Glu Phe Ala Pro Met Tyr Lys Ile Asn Tyr Ser Arg Asp Gly Thr Arg  
 115 120 125  
 Trp Ile Ser Trp Arg Asn Arg His Gly Lys Gln Val Leu Asp Gly Asn  
 130 135 140  
 Ser Asn Pro Tyr Asp Ile Phe Leu Lys Asp Leu Glu Pro Pro Ile Val  
 145 150 155 160  
 Ala Arg Phe Val Arg Phe Ile Pro Val Thr Asp His Ser Met Asn Val  
 165 170 175  
 Cys Met Arg Val Glu Leu Tyr Gly Cys Val Trp Leu Asp Gly Leu Val  
 180 185 190  
 Ser Tyr Asn Ala Pro Ala Gly Gln Gln Phe Val Leu Pro Gly Gly Ser  
 195 200 205  
 Ile Ile Tyr Leu Asn Asp Ser Val Tyr Asp Gly Ala Val Gly Tyr Ser  
 210 215 220  
 Met Thr Glu Gly Leu Gly Gln Leu Thr Asp Gly Val Ser Gly Leu Asp  
 225 230 235 240  
 Asp Phe Thr Gln Thr His Glu Tyr His Val Trp Pro Gly Tyr Asp Tyr  
 245 250 255  
 Val Gly Trp Arg Asn Glu Ser Ala Thr Asn Gly Tyr Ile Glu Ile Met  
 260 265 270  
 Phe Glu Phe Asp Arg Ile Arg Asn Phe Thr Thr Met Lys Val His Cys  
 275 280 285  
 Asn Asn Met Phe Ala Lys Gly Val Lys Ile Phe Lys Glu Val Gln Cys  
 290 295 300  
 Tyr Phe Arg Ser Glu Ala Ser Glu Trp Glu Pro Asn Ala Ile Ser Phe  
 305 310 315 320  
 Pro Leu Val Leu Asp Asp Val Asn Pro Ser Ala Arg Phe Val Thr Val  
 325 330 335

Pro Leu His His Arg Met Ala Ser Ala Ile Lys Cys Gln Tyr His Phe  
340 345 350

Ala Asp Thr Trp Met Met Phe Ser Glu Ile Thr Phe Gln Ser Asp Ala  
355 360 365

Ala Met Tyr Asn Asn Ser Glu Ala Leu Pro Thr Ser Pro Met Ala Pro  
370 375 380

Thr Thr Tyr Asp Pro Met Leu Lys Val Asp Asp Ser Asn Thr Arg Ile  
385 390 395 400

Leu Ile Gly Cys Leu Val Ala Ile Ile Phe Ile Leu Leu Ala Ile Ile  
405 410 415

Val Ile Ile Leu Trp Arg Gln Phe Trp Gln Lys Met Leu Glu Lys Ala  
420 425 430

Ser Arg Arg Met Leu Asp Asp Glu Met Thr Val Ser Leu Ser Leu Pro  
435 440 445

Ser Asp Ser Ser Met Phe Asn Asn Asn Arg Ser Ser Ser Pro Ser Glu  
450 455 460

Gln Gly Ser Asn Ser Thr Tyr Asp Arg Ile Phe Pro Leu Arg Pro Asp  
465 470 475 480

Tyr Gln Glu Pro Ser Arg Leu Ile Arg Lys Leu Pro Glu Phe Ala Pro  
485 490 495

Gly Glu Glu Glu Ser Gly Cys Ser Gly Val Val Lys Pro Val Gln Pro  
500 505 510

Ser Gly Pro Glu Gly Val Pro His Tyr Ala Glu Ala Asp Ile Val Asn  
515 520 525

Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ser Val Pro Ala Val Thr  
530 535 540

Met Asp Leu Leu Ser Gly Lys Asp Val Ala Val Glu Glu Phe Pro Arg  
545 550 555 560

Lys Leu Leu Thr Phe Lys Glu Lys Leu Gly Glu Gly Gln Phe Gly Glu  
565 570 575

Val His Leu Cys Glu Val Glu Gly Met Glu Lys Phe Lys Asp Lys Asp  
580 585 590

Phe Ala Leu Asp Val Ser Ala Asn Gln Pro Val Leu Val Ala Val Lys  
595 600 605

Met Leu Arg Ala Asp Ala Asn Lys Asn Ala Arg Asn Asp Phe Leu Lys  
610 615 620

Glu Ile Lys Ile Met Ser Arg Leu Lys Asp Pro Asn Ile Ile His Leu  
625 630 635 640



Leu Ser Val Cys Ile Thr Asp Asp Pro Leu Cys Met Ile Thr Glu Tyr  
 645 650 655  
 Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser Arg His Glu Pro Pro  
 660 665 670  
 Asn Ser Ser Ser Ser Asp Val Arg Thr Val Ser Tyr Thr Asn Leu Lys  
 675 680 685  
 Phe Met Ala Thr Gln Ile Ala Ser Gly Met Lys Tyr Leu Ser Ser Leu  
 690 695 700  
 Asn Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Lys  
 705 710 715 720  
 Asn Tyr Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg Asn Leu Tyr  
 725 730 735  
 Ser Gly Asp Tyr Tyr Arg Ile Gln Gly Arg Ala Val Leu Pro Ile Arg  
 740 745 750  
 Trp Met Ser Trp Glu Ser Ile Leu Leu Gly Lys Phe Thr Thr Ala Ser  
 755 760 765  
 Asp Val Trp Ala Phe Gly Val Thr Leu Trp Glu Thr Phe Thr Phe Cys  
 770 775 780  
 Gln Glu Gln Pro Tyr Ser Gln Leu Ser Asp Glu Gln Val Ile Glu Asn  
 785 790 795 800  
 Thr Gly Glu Phe Phe Arg Asp Gln Gly Arg Gln Thr Tyr Leu Pro Gln  
 805 810 815  
 Pro Ala Ile Cys Pro Asp Ser Val Tyr Lys Leu Met Leu Ser Cys Trp  
 820 825 830  
 Arg Arg Asp Thr Lys Asn Arg Pro Ser Phe Gln Glu Ile His Leu Leu  
 835 840 845  
 Leu Leu Gln Gln Gly Asp Glu  
 850 855

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Ala can be exchanged for any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Pro Ala Tyr  
1

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Tyr Ala Xaa Pro Xaa Xaa Xaa Pro Gly  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 6 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

His Arg Asp Leu Ala Ala  
1                    5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGAATTCCCA YMGNRAYYTN RCNRCNMG

28

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "Xaa can be either Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Asp Val Trp Ser Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGAATTCCYW YNSWGGTNTG SAGNST

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Asp Pro Ala Lys Asp Cys Arg Tyr Ala Leu Gly Met Gln Asp  
1 5 10 15

Arg Thr Ile

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Pro Pro Phe Ser Gln Leu His Arg Phe Leu Ala Glu Asp Ala Leu  
1                    5                    10                    15

Asn Thr Val

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Ala Met Ala Trp Glu Gly Glu Pro Met Arg His Asn Leu  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys Trp Ser Arg Glu Ser Glu Gln Arg Pro Pro Phe Ser Gln Leu His  
1                    5                    10                    15

Arg